Design, Synthesis, Structural and Functional Characterization of Novel Melanocortin Agonists Based on the Cyclotide Kalata B1*

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Background: Cyclotides are useful scaffolds to stabilize bioactive peptides.
Results: Four melanocortin analogues of kalata B1 were synthesized. One is a selective MC4R agonist.
Conclusion: The analogues retain the native kalata B1 scaffold and introduce a designed pharmacological activity, validating cyclotides as protein engineering scaffolds.
Significance: A novel type of melanocortin agonist has been developed, with potential as a drug lead for treating obesity.

Obesity is an increasingly important global health problem that lacks current treatment options. The melanocortin receptor 4 (MC4R) is a target for obesity therapies because its activation triggers appetite suppression and increases energy expenditure. Cyclotides have been suggested as scaffolds for the insertion and stabilization of pharmaceutically active peptides. In this study, we explored the development of appetite-reducing peptides by synthesizing MC4R agonists based on the insertion of the His-Phe-Arg-Trp sequence into the cyclotide kalata B1. The ability of the analogues to fold similarly to kalata B1 but display MC4R activity were investigated. Four peptides were synthesized using t-butoxycarbonyl peptide chemistry with a C-terminal thioester to facilitate backbone cyclization. The structures of the peptides were found to be similar to kalata B1, evaluated by Hage NMR chemical shifts. KB1(GHFRWG;23–28) had a Kᵢ of 29 nM at the MC4R and was 107 or 314 times more selective over this receptor than MC1R or MC5R, respectively, and had no detectable binding to MC3R. The peptide had higher affinity for the MC4R than the endogenous agonist, α-melanocyte stimulation hormone, but it was less potent at the MC4R, with an EC₅₀ of 580 nM for activation of the MC4R. In conclusion, we synthesized melanocortin analogues of kalata B1 that preserve the structural scaffold and display receptor binding and functional activity. KB1(GHFRWG;23–28) is potent and selective for the MC4R. This compound validates the use of cyclotides as scaffolds and has the potential to be a new lead for the treatment of obesity.

Obesity is an increasing problem world wide with 1.5 billion adults estimated to be overweight (body mass index above 25 kg/m²) and 500 million obese (body mass index above 30 kg/m²) in 2008 (1). These statistics are alarming given that obesity is associated with a variety of debilitating diseases, including type 2 diabetes, cardiovascular disease, and hypertension (2–4). To prevent or reduce obesity and the risk of related diseases, regular exercise and a healthy diet are very effective (5), but in high risk patients drug treatment is also necessary (6). Currently, only two drugs are approved for the treatment of obesity, i.e. orlistat and phentermine. The Food and Drug Administration withdrew sibutramine in 2010 because of increased risk of cardiovascular events (7). Although drugs currently on the market for other indications are undergoing clinical trials for their potential to treat obesity, there is still an urgent need for new drugs targeting the world-wide obesity problem.

One approach to the development of drugs for the treatment of obesity is to target the melanocortin system, which includes a family of five G-protein-coupled receptors, the melanocortin receptors (MCR), named MCR1–5 in the order of their discovery (8–12). The endogenous peptide agonists, adrenocorticotropic hormone and α-, β-, and γ-melanoctye-stimulating hormone (MSH), all derived from the precursor protein pro-opiomelanocortin, form part of the system, in addition to the inverse agonists agouti protein and agouti-related protein. The five MCRs are distributed throughout the body and are associated with a variety of physiological effects. MC1R is mainly present in melanocytes and melanoma cells (8, 9).

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MC2R is present in the adrenal cortex, where it regulates steroidogenesis, and is only activated by adrenocorticotropic hormone, in contrast to the other MCRs (8). MC3R is mainly expressed in the arcuate nucleus (13) but is also present in the gut (10). MC4R is found throughout the brain (14) and in the spinal cord and dorsal root ganglions (15). Stimulation of MC4R reduces food intake and increases the metabolic rate in mice (16), which makes it an interesting target for the treatment of obesity. MC5R is distributed throughout the body with high levels found in skeletal muscle, brain, and exocrine glands and has a variety of functions (12, 17, 18).

The MSH peptides and adrenocorticotropic hormone share the tetrapeptide His-Phe-Arg-Trp pharmacophore, which is the shortest peptide active on the MCRs (19). Various modifications to these peptides have been made to explore the role of individual amino acids. Substitution of Met with norleucine (Nle) and modifying the conformation of Phe to D-Phe in α-MSH (see Table 1) yielded a stable subnanomolar agonist named NDP-α-MSH (20). Additionally, it has been shown that the His-D-Phe-Arg-Trp tetrapeptide alone has nanomolar activity on the MC4R (21). In another study, a truncated analogue of the inverse agonist agouti-related protein was turned into a full agonist by exchanging the binding sequence with His-D-Phe-Arg-Trp (22). These findings suggest that it might be possible to graft the His-Phe-Arg-Trp sequence and related modified sequences into stable peptide frameworks to develop novel MCR agonists.

The concept of developing MC4R agonists for the treatment of obesity has been around for more than a decade, and agonists have been shown to have efficacy in rodent models of obesity (23). However, despite strenuous efforts, no compounds have reached clinical trials for the treatment of obesity. The similarity between the various MCRs, which makes it challenging to make selective agonists, and the generally low half-lives of peptides in vivo (24) have probably contributed to this lack of success.

Recent discoveries of naturally occurring stable peptides offer the potential to overcome some of the limitations of peptides as drug leads. In the mid-1990s, several ultra-stable peptides that had both a cyclic backbone and three disulfide bonds forming a cystine knot were discovered (25–28). The most extensively studied of these is the 29-residue peptide kalata B1 found in the African plant Oldenlandia affinis (26), which originally attracted attention because of its reported uterotonic activity (29). More recently, it has been reported to have antimicrobial (30) and cancer cell cytotoxic activity (31) as well as a range of other activities (32). Its biological function in the plant is thought to be as a host defense pesticidal agent, because it reduces the growth of the larvae of the crop pest Helicoverpa punctigera (33). Following additional discovery efforts (34–38) since these early studies, the group of cyclic cystine-knotted (CCK) peptides now includes several hundred sequences and has been given the name cyclotides (35, 39). They are exceptionally stable toward enzymatic or thermal degradation because of their cyclic backbone and cystine knot (26, 28, 40). Because of their stability and large sequence variation in nature, cyclotides have been suggested as promising scaffolds for the grafting of pharmacologically interesting peptides to stabilize them (35, 41). There are six backbone loops decorating the cystine knot core, and these offer opportunities for conformational control of a variety of peptide epitopes. In addition to being amenable to solid phase peptide synthesis (30, 42), cyclotide libraries have recently been expressed in bacterial cells (43), thus providing alternative routes to their manufacture.

There are currently only a few examples demonstrating the grafting of biologically active sequences into cyclotides or related acyclic cystine knot scaffolds. For example, Clark et al. (44) demonstrated that it was possible to substitute selected amino acids in loop 5 of kalata B1 to remove intrinsically hemolytic activity but retain the native fold, and later studies on this framework demonstrated efficacy for grafted antiangiogenic sequences (45) and bradykinin antagonists (46). Thongyoo et al. (47) changed the specificity of the trypsin inhibitor cyclotide, MCoTI-II, toward other proteases with one to three amino acid substitutions, and Chan et al. (48) reported a novel angiogenic agent based on this framework. In acyclic cystine-knotted peptides, Reiss et al. (49) successfully grafted platelet aggregation inhibiting sequences, and as mentioned above, agouti-related protein was turned into a full agonist on the melanocortin receptors (22).

In this study, kalata B1 was used as a scaffold for the insertion (grafting) of melanocortin receptor-activating sequences. The grafted sequences are shown in Fig. 1 along with the NMR-derived structure of kalata B1. These analogues have the potential to become leads for a new class of melanocortin receptor agonists for the treatment of obesity. More broadly, they will expand knowledge on the applicability of cyclotides as scaffolds.

**EXPERIMENTAL PROCEDURES**

**Peptide Synthesis**—Peptides were synthesized manually by Boc solid phase peptide synthesis on a Boc-Gly-phenylacetamido-methyl resin using 2-(1-H-benzotriazol-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphatate or 2-(6-chloro-1-H-benzotriazol-1-yl)-1,1,3,3-tetramethylaminium hexafluorophosphatate as coupling reagents, as described previously (44). Mercaptopropionic acid was used as a linker to facilitate backbone cyclization by native chemical ligation (50). Peptides were cleaved from the resin using hydrogen fluoride/cresol/thiocresol (50:4:1 v/v/v), precipitated in diethyl ether, and lyophilized. The crude peptides were purified using HPLC with a gradient of 25–45% solvent B (90% acetonitrile, 0.1% TFA in water) against solvent A (0.1% TFA in water) over 40 min. A Phenomenex C18 column was used and absorbance measured at 280 nm. Backbone cyclization and disulfide bonds were formed using 0.1 M ammonium bicarbonate (pH 8.2), isopropyl alcohol (50:50, v/v) buffer for 48 h, at a peptide concentration of 0.2 mg/ml. At 0 and 24 h, 1 mM reduced glutathione was added. The oxidized peptides were purified on HPLC with 30–50% solvent B over 60 min. The peptides were characterized using electrospray ionization mass spectrometry; the purity was determined by RP-ultra-performance liquid chromatography, and the peptides were quantified using a chemiluminescent nitrogen detector (51).
**NMR**—Peptides were dissolved at a concentration of \(-1 \text{ mmol/L}\) in 10% D_2O and 90% H_2O. Spectra were recorded at 298 K on a Bruker AVANCE 600 MHz NMR spectrometer. Two-dimensional spectra included TOCSY, NOESY, and DQF-COSY. The mixing times for the TOCSY and NOESY spectra were 80 and 200 ms, respectively. The processed spectra were analyzed using the program CcPnMR Analysis, University of Cambridge, UK. Three-dimensional structures were calculated from the recorded two-dimensional spectra using CYANA as described previously (52). Structures were analyzed using Molprobity and PROMOTIF (53) and displayed using MolMol (54) and PyMol (55). Structures and chemical shifts have been deposited in the Protein Data Bank (Protein Data Bank code 2lur) and Biomagnetic Resonance Bank (BMRB ID 18536), respectively.

**Melanocortin Assays**—Melanocortin receptor binding assays were conducted as described previously (56). Each assay was performed in duplicate, and three assays were done on each receptor. Peptides (3 pmol to 3 nmol) were incubated with homogenized membranes from baby hamster kidney cells expressing the various MCRs and ^125^I-NDP-\(\alpha\)-MSH (around 60,000 counts/min). The incubation was stopped after 1 h by filtration through polyethyleneimine-treated filter plates. Scintillation liquid was added to the plates, and the radioactivity was counted.

The cAMP activity assays were conducted on baby hamster kidney cells expressing the MC4R, using the FlashPlate™ assay as described previously (56). Cells and peptide (100 fM to 100 nM) were incubated and shaken for 30 min at room temperature. Detection mixture was added according to FlashPlate protocol, shaken for 30 min, and incubated overnight. The amount of cAMP produced was measured by displacement of radiolabeled cAMP bound to anti-cAMP antibodies in accordance with the FlashPlate protocol.

The data analyses from the receptor assays were performed as described previously (56), using the program GraphPad Prism, GraphPad Software. IC_{50} values were calculated using a nonlinear regression model, and K_I values were calculated from the IC_{50} values. The potency at the MC4R was determined as EC_{50} values, calculated by nonlinear regression of the activity assay data.

**Enzymatic Cleavage Assays**—Peptides were incubated with chymotrypsin (1:5 w/w enzyme/peptide ratio) at 37 °C. For \(\alpha\)-MSH, the ratio was 1:10 w/w enzyme/peptide to have close to equal molar ratios for all peptides. Samples were aliquoted out and quenched with TFA before analysis on ultra-performance liquid chromatography. Peak heights were used to calculate the amount of intact peptide.

**RESULTS**

**Design, Synthesis, and Characterization of the Grafted Peptides**—Four melanocortin analogues of kalata B1 were synthesized using solid phase Boc chemistry. The sequences of the peptides are shown in Table 1. They are named to reflect the grafted epitopes incorporated into the kalata B1 (kB1) sequence. For example, kB1(GHRW;24–27) indicates replacement of residues 24–27 in loop 6 of kalata B1 (kB1) with the HFRW (His-Phe-Arg-Trp) tetrapeptide sequence. In this case, the tetrapeptide is flanked by the remaining native amino acids in loop 6, i.e. T at the N-terminal side and PV at the C-terminal side, making the total composition of loop 6 THFRWPV in place of the native TRNGLPV. To account for the possibility that direct replacements might constrain the bioactive tetrapeptide in a nonactive conformation, other grafts were made where flanking glycine residues were used in place of the native kalata B1 residues.

The peptides were assembled attached to a C-terminal mercaptopropionic acid linker to facilitate subsequent cyclization of the termini. The linear precursor peptides were synthesized with Val\(^{24}\) as the C terminus, because this allowed the synthesis of one batch of resin to which was coupled the first 22 amino acids common to all analogues. This batch was subsequently split to continue separate synthesis of the differing parts of the four analogues. Loop 6 was chosen as the site for grafting the melanocortin sequence, because it is the largest of the inter-cysteine loops in kalata B1. In addition, the structure of kalata B1 shown in Fig. 1 indicates that the other loops are not in close proximity with loop 6 and therefore are not likely to interfere with the presentation of the grafted melanocortin sequence to the MCRs.

The peptides were cleaved from the resin and then oxidized and cyclized in a single step at 0.2 mg/ml concentration in a 0.1 M ammonium bicarbonate (pH 8.2), isopropryl alcohol (50:50, v/v) buffer for 48 h with 1 mm reduced glutathione added at 0
Novel Melanocortin Agonists Based on the Kalata B1 Scaffold

Peptides are shown in Fig. 2. The peaks corresponding to the correctly folded peptides are marked with an asterisk.

and 24 h. Chromatograms from the purification of the folded peptides are shown in Fig. 2.

The late eluting peaks were purified and analyzed by NMR spectroscopy to confirm that the native fold was present. A comparison of the Hα chemical shifts of the grafted peptides with the native peptide is shown in Fig. 3. The comparison indicates that the overall structures of the peptides are similar. The only Hα chemical shift differences larger than 0.2 ppm were found for Val29, which is the C-terminal neighbor to the grafted sequence, Cys1, which is bound to Val29, and Cys15, which forms a disulfide with Cys1.

The grafted sequence has several large hydrophobic residues, including His, Phe, and Trp as shown in Fig. 5. In addition, residues 5–8 form a type I β-turn, and residues 10–12 and 12–14 form inverse γ-turns. Comparison of the structure of kB1(GHFRWG;23–28) with the native kalata B1 framework indicates that the overall fold is maintained. The cyclic cystine knot motif and β-hairpin are the defining structural features of the cyclotides, and both are present in kB1(GHFRWG;23–28), despite the structure changes in loop 6.

The introduction of non-native sequences into the CCK scaffold can sometimes lead to disordered loops (45, 48). However, for kB1(GHFRWG;23–28) the grafted loop 6 is as well defined as the other loops, with order parameters >0.93 for the φ and ψ angles over the whole molecule.

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kB1(GHFRWG;23–28) has two additional potential chymotrypsin cleavage sites in the grafted sequence, so the observed resistance to proteolysis is a significant finding. Finally, H9251-MSH completely degraded within 10 min.

**TABLE 2**

<table>
<thead>
<tr>
<th>Peptide</th>
<th>hMC1R, pK_i</th>
<th>hMC3R, pK_i</th>
<th>hMC4R, pK_i</th>
<th>hMC4R, cAMP pEC_50</th>
<th>hMC5R, pK_i</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kalata B1</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>kB1(GHFRWG;23–28)</td>
<td>5.50 ± 0.09</td>
<td>7.53 ± 0.28</td>
<td>6.24 ± 0.08</td>
<td>5.04 ± 0.14</td>
<td>NA</td>
</tr>
<tr>
<td>kβ1(HFRW;24–27)</td>
<td>6.37 ± 0.06</td>
<td>6.59 ± 0.15</td>
<td>5.30 ± 0.04</td>
<td>5.00 ± 0.00</td>
<td>NA</td>
</tr>
<tr>
<td>α-MSH</td>
<td>9.16 ± 0.05</td>
<td>7.41 ± 0.26</td>
<td>8.44 ± 0.26</td>
<td>6.75 ± 0.16</td>
<td>NA</td>
</tr>
</tbody>
</table>

**DISCUSSION**

In this study we used the kalata B1 cyclotide scaffold to design a novel agonist for the MC4R. This analogue (kB1(GHFRWG;23–28)) also showed selectivity over other

**FIGURE 3.** 1H chemical shifts of the four synthesized peptides and kalata B1. The numbers corresponding to cysteine residues are highlighted in boldface.

**FIGURE 4.** MC4R binding assays for kB1(GHFRWG;23–28), kalata B1 and α-MSH. Each assay was performed in duplicate. Cell membranes expressing the MC4R were incubated with 125I-NDP-α-MSH and the synthesized peptides. The amount of radioactivity from bound 125I-NDP-α-MSH was counted, and K_i values were calculated. Data points are average values from the assays, and S.E. values are indicated with error bars.

**TABLE 3**

<table>
<thead>
<tr>
<th>NMR distance and dihedral constraints</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Distance constraints</td>
<td></td>
</tr>
<tr>
<td>Total NOE</td>
<td>291</td>
</tr>
<tr>
<td>Short range ($i-j&lt;1$)</td>
<td>202</td>
</tr>
<tr>
<td>Medium range ($1(i-j)&lt;5$)</td>
<td>42</td>
</tr>
<tr>
<td>Long range ($</td>
<td>i-j</td>
</tr>
<tr>
<td>Dihedral angle constraints</td>
<td>12</td>
</tr>
<tr>
<td>ϕ</td>
<td></td>
</tr>
</tbody>
</table>

**Structure statistics**

| CYANA target function          | 1.02 ± 0.07 |
| Violations (mean ± S.D.)       | 0.01 ± 0.002 Å |
| Distance constraints, r.m.s.d. | 1.45 ± 0.12°  |
| Dihedral angle violations      | 0.26 Å       |
| Max. dihedral angle violation  | 1.01°        |
| Average pairwise r.m.s.d.*     | 0.41 ± 0.11 Å |
| Backbone                        | 0.84 ± 0.18 Å |
| Heavy                           |               |

**Ramachandran statistics**

| Residues most favored regions   | 49.5% |
| Residues in additionally allowed regions | 50.5% |

*Pairwise root mean square deviation (r.m.s.d.) was calculated from the 20 structures with the lowest target function.
MCRs tested, highlighting the potential of the CCK scaffold for targeting specific interactions implicated in the regulation of appetite and energy homeostasis and providing a possible lead molecule for the treatment of obesity. Interestingly, kB1(GHFRWG;23–28) showed higher affinity for the MC4R compared with the native agonist α-MSH, but it was not as potent functionally. It appears likely that kB1(GHFRWG;23–28) has stronger binding to the active site than α-MSH, but due to the placement of the pharmacophore within the kalata B1 scaffold and possible steric clashes with the receptor, it is not able to induce a similar conformational change in the receptor, which is required for full activation of the cAMP cascade. Nevertheless, significant (sub-micromolar) activation of the cAMP response was observed. This successful example of grafting a function into a cyclotide adds to a growing body of evidence that the CCK framework can accommodate a diverse range of bioactivities.

Four analogues of kalata B1 were synthesized using Boc chemistry and generally folded well using the oxidation conditions previously established for native kalata B1 (Fig. 2). All of the analogues retained the native fold based on analysis with NMR spectroscopy. Even though six of the seven residues in loop 6 were replaced, the CCK holds the remaining loops in place and allows these changes in loop 6. The grafted sequence is significantly more hydrophobic than sequences previously grafted into this framework, and this study expands the known sequence diversity accommodated by the cyclotide scaffold (44–46, 48), and in particular highlights the tolerance of loop 6 to changes. This tolerance is further demonstrated by observations that loop 6 can be truncated and opened to produce acyclic cystine knot derivatives that maintain the same global fold as kalata B1 (57). In essence, the exposed loops of the CCK framework can be regarded as “plug and play” cassettes that can be substituted to introduce a desired biological activity.

Interestingly, kB1(GHFRWG;23–28), the D-Phe25 analogue of kB1(GHFRWG;23–28) bound with lower affinity to the MCRs than the all-L graft. This was surprising because D-Phe analogues of short linear peptides are known to have higher affinity for the MCRs compared with the L-Phe analogues (20). The locked conformation of the pharmacophore in loop 6 of kalata B1 could change the presentation to the active site of the receptors and consequently be an explanation for this observation. There is clearly potential for further optimization of the bioactive epitope, and these studies are planned in our laboratory.
NMR spectra for kB1(HFRW;24–27) and kB1(HFRW;24–27) revealed that two conformations were present. This conformational heterogeneity appears to be related to cis/trans-isomerization around Pro28. The major conformation, based on inter-residue cross-peaks was the cis-conformation. This was confirmed by a strong Hα-Hα cross-peak between Trp27 and Pro28. The cis-Pro conformation is consistent with what has previously been described for the Trp9–Pro20 bond in kalata B1 (35, 58). The strong Hα-Hα cross-peak between Trp19 and Pro20 was observed in all peptides, whereas a Hα-Hδ cross-peak was observed for the Thr12–Pro13 bond. The cis-Pro28 bond causes a conceptual twist in the backbone, which defines the Möbius family of cyclotides (35). The additional twist caused by the cis-Pro28 bond changes the topology of kB1(HFRW;24–27) and kB1(HFRW;24–27). This could be part of the reason why they did not bind to the MCRs, because a twist in the backbone around the pharmacophore changes the presentation of the side chains at the active site of the receptors. Besides the conformational change, it is also possible that the side chains of Thr23 and Pro28 in kB1(HFRW;24–27) and kB1(HFRW;24–27) affect the binding of the pharmacophore to the active site of the MCRs negatively compared with Gly23 and Gly28 in kB1(GHFRWG;23–28) and kB1(GHFRWG;23–28), which due to their lack of side chain would interfere less with the active site.

The intrinsic resistance of α-MSH to proteolytic degradation is very low but can be somewhat increased by engineering a delivery might be achieved with other examples of kalata B1 (35, 58). The strong Hα-Hα cross-peak between Trp27 and Pro28. The cis-Pro conformation is consistent with what has previously been described for the Trp9–Pro20 bond in kalata B1 (35, 58). The strong Hα-Hα cross-peak between Trp19 and Pro20 was observed in all peptides, whereas a Hα-Hδ cross-peak was observed for the Thr12–Pro13 bond. The cis-Pro28 bond causes a conceptual twist in the backbone, which defines the Möbius family of cyclotides (35). The additional twist caused by the cis-Pro28 bond changes the topology of kB1(HFRW;24–27) and kB1(HFRW;24–27). This could be part of the reason why they did not bind to the MCRs, because a twist in the backbone around the pharmacophore changes the presentation of the side chains at the active site of the receptors. Besides the conformational change, it is also possible that the side chains of Thr23 and Pro28 in kB1(HFRW;24–27) and kB1(HFRW;24–27) affect the binding of the pharmacophore to the active site of the MCRs negatively compared with Gly23 and Gly28 in kB1(GHFRWG;23–28) and kB1(GHFRWG;23–28), which due to their lack of side chain would interfere less with the active site.

The intrinsic resistance of α-MSH to proteolytic degradation is very low but can be somewhat increased by engineering a single disulfide in the sequence (59). Kalata B1 has been demonstrated to have significantly increased stability toward enzymatic degradation compared with noncystine-knotted analogues, linear cystine-knotted peptides, and noncyclic peptides (40). It was of interest to determine whether the target-grafting site.

REFERENCES

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